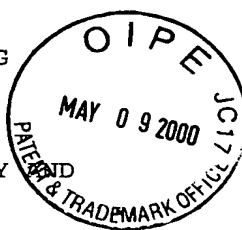


SEQUENCE LISTING



<110> INSTITUT PASTEUR

<120> HYBRID PROTEINS THAT MIGRATE RETROGRADELY
TRANSYNAPTICALLY INTO THE CNS

<130> B4001_AD/CAL

<140> PCT/EP98/05113

<141> 1998-08-12

<150> 60/055,615

<151> 1997-08-14

<150> 60/065,236

<151> 1997-11-13

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(49)

<223> sequence used to generate PCR fragments

<400> 1

ccccccgggc caccatgggt ttttcaacac caattccatt ttcttattc

49

<210> 2

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 2

ctaaaccagt aatttctg

18

<210> 3

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 3

aattatggac tttaaaagat tccgc

25

<210> 4
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 4
 ggccattataa cctactctta gaat 24

<210> 5
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 5
 aatgccttta ataactctga tagaaat 27

<210> 6
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 6
 cccccgggc atatgtcatg aacatatcaa tctgtttaat c 41

<210> 7
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 7
 ctgaatatcg acggtttcca tatg 24

<210> 8
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 8
 ggccagtctcg agtctagacc atggcttttt gacaccagac 40

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: linker

<400> 9
 catgactggg gatccccagt 20

<210> 10
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 10
 tatgataaaa atgcattctt agga 24

<210> 11
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <221> misc_feature
 <222> (1)..(37)
 <223> sequence used to change NcoI into BamHI
 restriction site

<400> 11
 tggagtcgac gctagcagga tcatttgtcc atccttc 37

<210> 12
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: linker

<400> 12
 gatatcggcg cgccagc 17

<210> 13
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: linker

<400> 13

tggcgcgccg atatcgc

17

<210> 14

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: linker

<220>

<221> misc_feature

<222> (1)..(14)

<223> sequence used to change XhoI into AscI restriction site

<400> 14

tcgatggcgc gccca

14

<210> 15

<211> 1600

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA

<220>

<221> CDS

<222> (88)..(1476)

<220>

<221> misc_feature

<222> (1)..(1600)

<223> sequence isolated from a Clostridium Tetani strain using PCR

<400> 15

ggaaacagct atgacatga ttacgccaag ctcgaaatta accctcacta aagggaacaa 60

aagctggagc tcggtaccgc ggccacc atg gtt ttt tca aca cca att cca ttt 114

Met Val Phe Ser Thr Pro Ile Pro Phe

1

5

tct tat tct aaa aat ctg gat tgt tgg gtt gat aat gaa gaa gat ata 162

Ser Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile

10

15

20

25

gat gtt ata tta aaa aag agt aca att tta aat tta gat att aat aat 210

Asp Val Ile Leu Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn

30

35

40

gat att ata tca gat ata tct ggg ttt aat tca tct gta ata aca tat 258

Asp Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr

45

50

55

cca gat gct caa ttg gtg ccc gga ata aat ggc aaa gca ata cat tta	306
Pro Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu	
60 65 70	
gta aac aat gaa tct tct gaa gtt ata gtg cat aaa gct atg gat att	354
Val Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile	
75 80 85	
gaa tat aat gat atg ttt aat aat ttt acc gtt agc ttt tgg ttg agg	402
Glu Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg	
90 95 100 105	
gtt cct aaa gta tct gct agt cat tta gaa caa tat ggc aca aat gag	450
Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu	
110 115 120	
tat tca ata att agc tct atg aaa aaa cat agt cta tca ata gga tct	498
Tyr Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser	
125 130 135	
ggg tgg agt gta tca ctt aaa ggt aat aac tta ata tgg act tta aaa	546
Gly Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys	
140 145 150	
gat tcc gcg gga gaa gtt aga caa ata act ttt agg gat tta cct gat	594
Asp Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp	
155 160 165	
aaa ttt aat gct tat tta gca aat aaa tgg gtt ttt ata act att act	642
Lys Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr	
170 175 180 185	
aat gat aga tta tct tct gct aat ttg tat ata aat gga gta ctt atg	690
Asn Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met	
190 195 200	
gga agt gca gaa att act ggt tta gga gct att aga gag gat aat aat	738
Gly Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn	
205 210 215	
ata aca tta aaa cta gat aga tgt aat aat aat aat caa tac gtt tct	786
Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser	
220 225 230	
att gat aaa ttt agg ata ttt tgc aaa gca tta aat cca aaa gag att	834
Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile	
235 240 245	
gaa aaa tta tac aca agt tat tta tct ata acc ttt tta aga gac ttc	882
Glu Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe	
250 255 260 265	
tgg gga aac cct tta cga tat gat aca gaa tat tat tta ata cca gta	930
Trp Gly Asn Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile Pro Val	
270 275 280	
gct tct agt tct aaa gat gtt caa ttg aaa aat ata aca gat tat atg	978
Ala Ser Ser Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp Tyr Met	
285 290 295	

10		15		20		25
Asp Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn	30		35		40	
Asp Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr	45		50		55	
Pro Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu	60		65		70	
Val Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile	75		80		85	
Glu Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg	90		95		100	105
Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu	110		115		120	
Tyr Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser	125		130		135	
Gly Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys	140		145		150	
Asp Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp	155		160		165	
Lys Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr	170		175		180	185
Asn Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met	190		195		200	
Gly Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn	205		210		215	
Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser	220		225		230	
Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile	235		240		245	
Glu Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe	250		255		260	265
Trp Gly Asn Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile Pro Val	270		275		280	
Ala Ser Ser Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp Tyr Met	285		290		295	
Tyr Leu Thr Asn Ala Pro Ser Tyr Thr Asn Gly Lys Leu Asn Ile Tyr	300		305		310	
Tyr Arg Arg Leu Tyr Asn Gly Leu Lys Phe Ile Ile Lys Arg Tyr Thr	315		320		325	
Pro Asn Asn Glu Ile Asp Ser Phe Val Lys Ser Gly Asp Phe Ile Lys	330		335		340	345

Leu Tyr Val Ser Tyr Asn Asn Asn Glu His Ile Val Gly Tyr Pro Lys
 350 355 360
 Asp Gly Asn Ala Phe Asn Asn Leu Asp Arg Ile Leu Arg Val Gly Tyr
 365 370 375
 Asn Ala Pro Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu
 380 385 390
 Arg Asp Leu Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp Lys
 395 400 405
 Asn Ala Ser Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly Asn
 410 415 420 425
 Asp Pro Asn Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn His
 430 435 440
 Leu Lys Asp Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr Asp
 445 450 455
 Glu Gly Trp Thr Asn Asp
 460